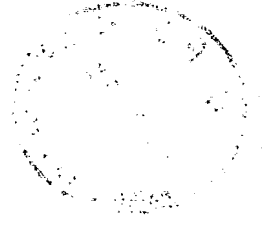


1	AGCAGACAGAGGACTCTCATTAAGGAAGG	TGTCCTGTGCCCTGACCCCTACAAGATGCCA	59
		MetPro	2
60	AGAGAAAGATGCTCACTTCATCTATGGTTAC	CCCAAGAAGGGGCACGGCCACTCTTACACC	119
3	ArgGluAspAlaHisPheIleTyrGlyTyr	ProLysLysGlyHisGlyHisSerTyrThr	22
120	ACGGCTGAAGAGGGCCGCTGGGATCGGCATC	CTGACAGTGATCCTGGGAGTCTTACTGCTC	180
23	ThrAlaGluGluAlaAlaGlyIleGlyIle	<u>LeuThrValIleLeuGlyValLeuLeuLeu</u>	43
181	ATCGGCTGTTGGTATTGTAGAAGACGAAAT	GGATACAGAGCCTTGATGGATAAAAGTCTT	239
44	<u>IleGlyCysTrpTyrCysArgArgArgAsn</u>	GlyTyrArgAlaLeuMetAspLysSerLeu	62
240	CATGTTGGCACTCAATGTGCCCTTAACAAGA	AGATGCCCAACAAGAAGGGTTTGATCATCGG	300
63	HisValGlyThrGlnCysAlaLeuThrArg	ArgCysProGlnGluGlyPheAspHisArg	83
301	GACAGCAAAGTGCTCTCTTCAAGAGAAAAAC	TGTGAACCTGTGGTTCCTCCCAATGCTCCACCT	359
84	AspSerLysValSerLeuGlnGluLysAsn	CysGluProValProAsnAlaProPro	102
360	GCTTATGAGAAACTCTCTGCAGAACAGTCA	CCACCACCTTATTACCTTAAGAGCCAGCG	420
103	AlaTyrGluLysLeuSerAlaGluGlnSer	ProProProTyrSerPro	118
421	AGACACCTGAGACATGCTGAAATTATTCT	CTCACACTTTTGCTTGAATTTAATACAGAC	479

FIG. 1A

00000000.001601

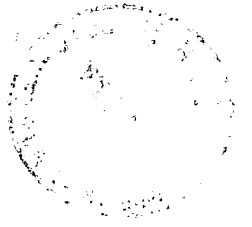
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480 ATCTAATGTTCTCCTTTTGGAAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC 540
541 AGTGTTAAAAATTTTAGTAGGTCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA 599
600 TATTAAATTGGGAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA 660
661 GGTAATGTTAGTAAATCCATGGTGTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT 719
720 GGGGCCATCCAATTTCTCTTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTTCG 780
781 AACCTTGACCGACATGAACGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG 839
840 GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT 900
901 CAGCAATGTCTCTTTTGTGCTCTAAAAATCT ATTATACTACAATAATAATATTTGTAAGATC 959
960 CTATAGCTCTTTTCTTTTGTGAGATGGAGTTT CGCTTTTGTGCCCCAGGCTGGAGTGCAATG 1020
1021 GCGCGATCTTGGCTCACCATAAACCTCCGCC TCCAGGTTCAAGCAATTCTCCTGCCCTTAG 1079
1080 CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTT 1140
1141 AGTAGAGACGGGGTTTCTCCATGTTGTCA GGCTGTTCTCAAACTCCTGACCTCAGGTGA 1199
1200 TCTGCCCCCTCAGCCTCCCAAAGTCTGG AATTACAGGCGTGAGCCACCCAGCCTGGCT 1260
1261 GGATCCTATATCTTAGTAAGACATAAAC GCAGTCTAATTACATTTTCACTTCAAGGCTC 1319
1320 AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACAGAAATTTGTTAGAGGATTT 1380
1381 AAATAAGTAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCCTTAAATG 1439
1440 TACCTATGGCAATTTAGCTCTCTTGGGTT CCAATCCCTCTCACAAAGAATGTGCAGAAG 1500
1501 AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAA 1559

FIG. 1B

00000000, 1016001



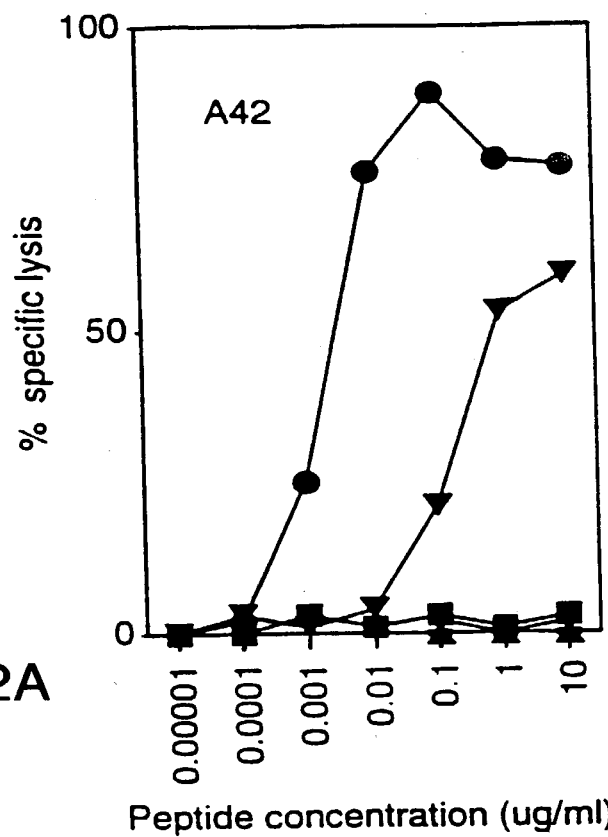
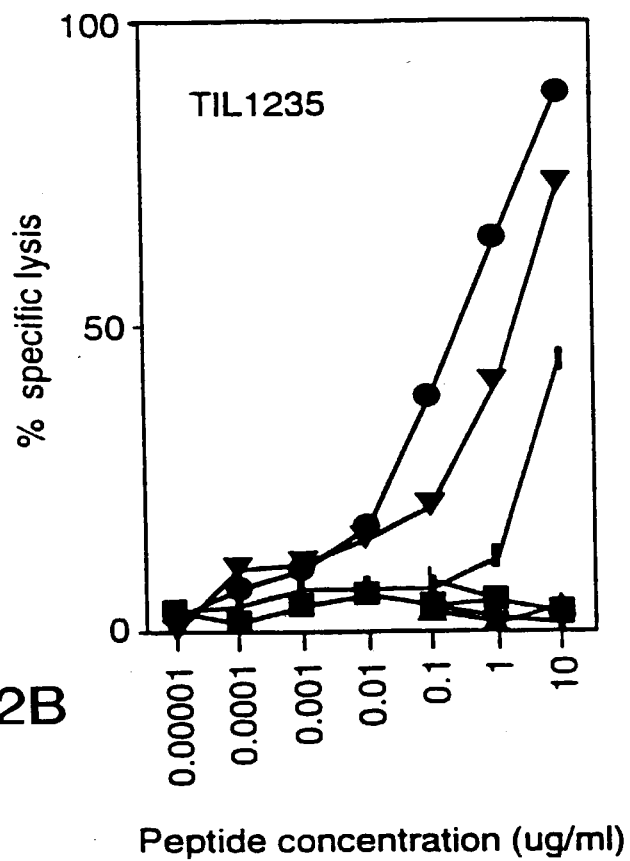


FIG. 2B



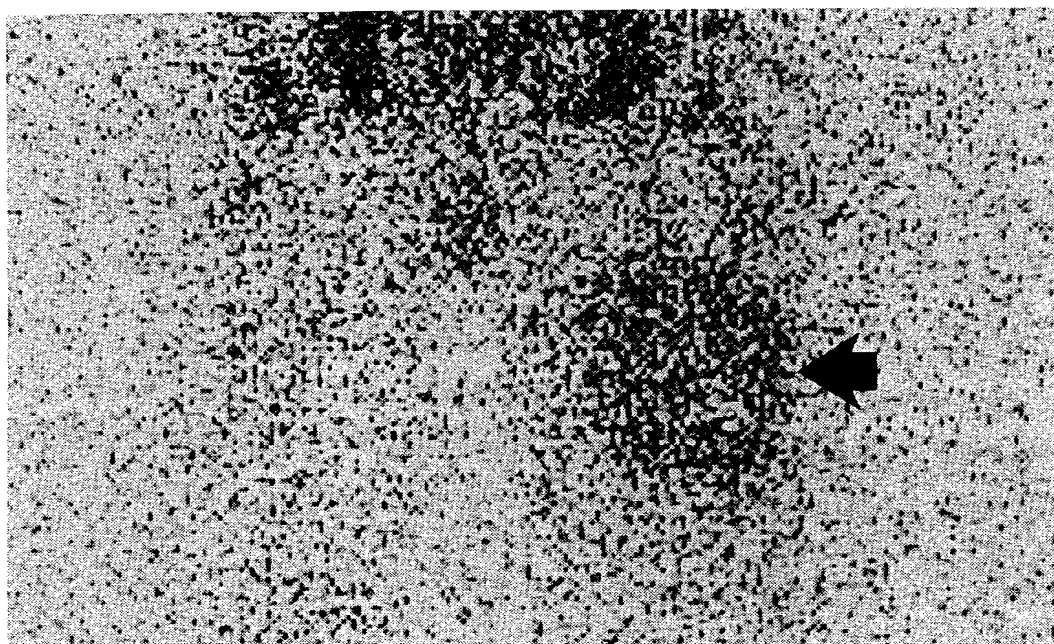


FIG. 3A

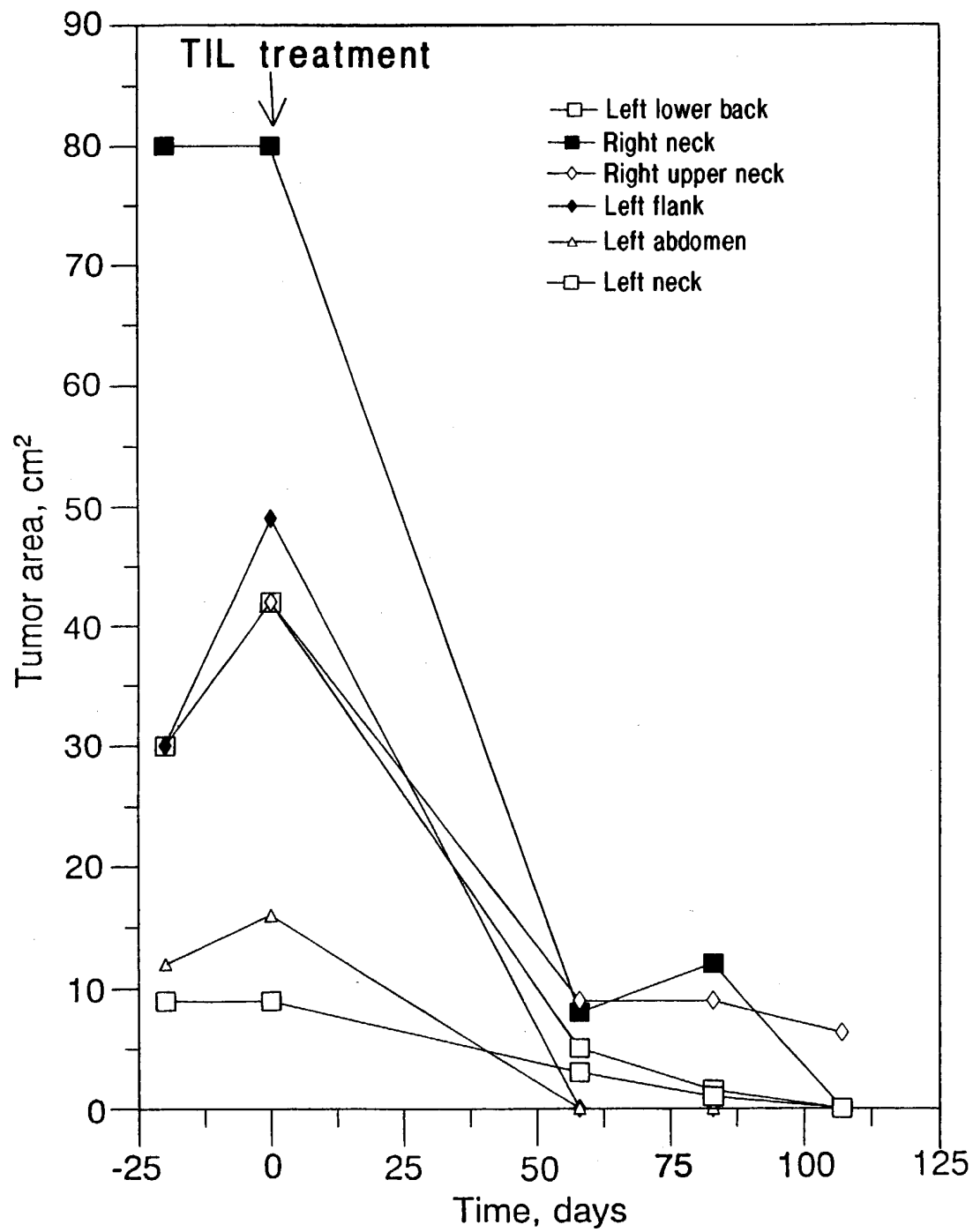


FIG. 3B

GTCGACGGCC	ATTACCAATC	GCGACCGGGA	AGAACACAAT	40
GGATCTGGTG	CTAAAAAGAT	GCCTTCTTCA	TTTGGCTGTG	80
ATAGGTGCTT	TGCTGGCTGT	GGGGGCTACA	AAAGTACCCA	120
GAAACCAGGA	CTGGCTTGGT	GTCTCAAGGC	AACTCAGAAC	160
CAAAGCCTGG	AACAGGCAGC	TGTATCCAGA	GTGGACAGAA	200
CCCAGAGAC	TTGACTGCTG	GAGAGGTGGT	CAAGTGTCCC	240
TCAAGGTCAG	TAATGATGGG	CCTACACTGA	TTGGTGCAAA	280
TGCCTCCTTC	TCTATTGCCT	TGAACTTCCC	TGGAAGCCAA	320
AAGGTATTGC	CAGATGGGCA	GGTTATCTGG	GTCAACAATA	360
CCATCATCAA	TGGGAGCCAG	GTGTGGGGAG	GACAGCCAGT	400
GTATCCCCAG	GAAACTGACG	ATGCCTGCAT	CTTCCCTGAT	440
GGTGGACCTT	GCCCATCTGG	CTCTTGGTCT	CAGAAGAGAA	480
GCTTTGTTTA	TGTCTGGAAG	ACCTGGGGCC	AATACTGGCA	520
ATTTCTAGGG	GGCCCAGTGT	CTGGGCTGAG	CATTGGGACA	560
GGCAGGGCAA	TGCTGGGCAC	ACACACCATG	GAAGTGA CTG	600
TCTACCATCG	CCGGGGATCC	CGGAGCTATG	TGCCTCTTGC	640
TCATTCCAGC	TCAGCCTTCA	CCATTACTGA	CCAGGTGCCT	680
TTCTCCGTGA	GCGTGTCCCA	GTTGCGGGCC	TTGGATGGAG	720
GGAACAAGCA	CTTCCTGAGA	AATCAGCCTC	TGACCTTTGC	760
CCTCCAGCTC	CATGACCCCA	GTGGCTATCT	GGCTGAAGCT	800
GACCTCTCCT	ACACCTGGGA	CTTTGGAGAC	AGTAGTGGAA	840
CCCTGATCTC	TCGGGCACTT	GTGGTCACTC	ATACTTACCT	880
GGAGCCTGGC	CCAGTCACTG	CCCAGGTGGT	CCTGCAGGCT	920
GCCATTCCCTC	TCACCTCCTG	TGGCTCCTCC	CCAGTTCCAG	960
GCACCACAGA	TGGGCACAGG	CCAACTGCAG	AGGCCCTAA	1000
CACCACAGCT	GGCCAAGTGC	CTACTACAGA	AGTTGTGGGT	1040
ACTACACCTG	GTCAGGCGCC	AACTGCAGAG	CCCTCTGGAA	1080
CCACATCTGT	GCAGGTGCCA	ACCACTGAAG	TCATAAGCAC	1120

FIG. 4A



TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIG. 4B



```

1  MDLVLRCLL  HLAVIGALLA  VGATKVPRNQ  DWLGVSRLR  TKAWNRLYP
51  EWTEAQLDC  WRGGQVSLKV  SNDGPTLGA  NASFSIALNF  PGSQKVLDPG
101 QVIWVNTII  NGSQVWGGQP  VYPQETDDAC  IFPDGGPCPS  GSWSQKRSFV
151 YVWKTWGQYW  QFLGGPVSGL  SIGTGRAMLG  THTMEVTVYH  RRGSRSYVPL
201 AHSSSAFTIT  DQVPFSVSVS  QLRALDGGNK  HFLRNQPLTF  ALQLHDPSTY
251 LAEADLSYTW  DFGDSSGTLI  SRALVVTHTY  LEPGPVTAQV  VLQAAIPLTS
301 CGSSPVPGTT  DGHRPTAEAP  NTTAGQVPTT  EVVGTTPGQA  PTAEPSGTTT
351 VQVPTTEVIS  TAPVQMPTAE  STGMTPEKVP  VSEVMGTTLA  EMSTPEATGM
401 TPAEVSIVVL  SGTAAQVTT  TEWVETTARE  LPIPEPEGPD  ASSIMSTESI
451 TGSIGPLLDG  TATLRLVKRQ  VPLDCVLYRY  GSFSVTLDIV  QGIESAEILQ
501 AVPSGEGDAF  ELTVSCQGGL  PKEACMEISS  PGCQPPAQL  CQVLPSPAC
551 QLVLHQILKG  GSGTYCLNVS  LADTNSLAVV  STQLIMPGQE  AGLGQVPLIV
601 GILLVLMVV  LASLIYRRRL  MKQDFSVPQL  PHSSSHWLRL  PRIFCSCPIG
651 ENSPLLSGQQ  V

```

FIG. 5A

```

Pme117      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20         M-----V-----Q-----L-----
gp100        M-----V-----Q-----L-----
cDNA25FL     M-----F-----Q-----L-----
cDNA25TR     Q-----L-----PPQWAAGLSTLI
              1       162       236       274       588       649

```

FIG. 5B

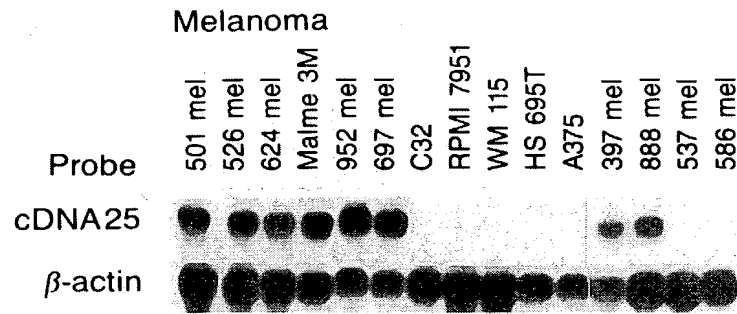
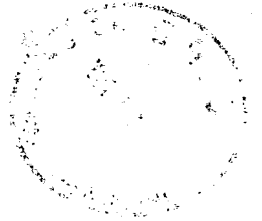


FIG. 6A

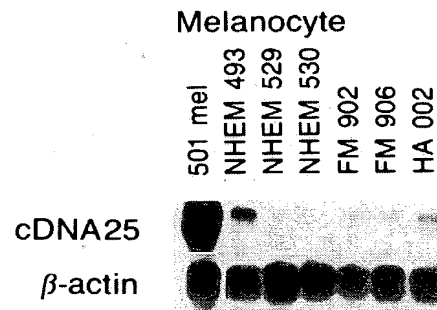


FIG. 6B

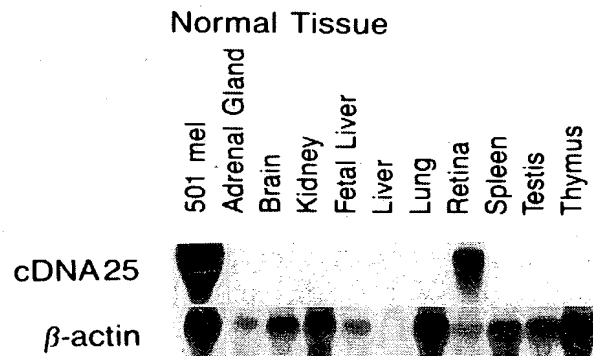


FIG. 6C